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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                         Database
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                             seq length: 0
seq length: 2000000000
PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                               March 1, 2001, 15:52:23; Search time 170.72 Seconds (without alignments) 264.889 Million cell updates/sec
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Gapop 10.0 ,
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3532
                                                                                                                                                                                                                                                                      195891 seqs, 67900655 residues
                                                                                                                                                                                                                                                                                                                                                             1 MAINTSNLCSLLFLLSLFLL.....SSRSTKQQQPLVSILDFVGF
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	% Query Match	% Query Match Length [	BB	ID	Description
_ ;	1191.5	33.7	810	2	T44430	protein PV100 (imp
2	1142	32.3	566	N	S22477	vicilia precursor
ω	1092	30.9	605	N	806398	alpha-globulin typ
4	1083.5	30.7	588	_	FWCNAB	alpha-qlobulin B p
5	1022.5	28.9	509	Ν	S08059	ţ
6	902	25.5	573	ν	A53234	globulin-1s, GLB1s
7	895	25.3	582	N	B53234	vicilin-like stora
8	875	24.8	637	2	S35221	globulin Beg1 prec
9	872.5	24.7	639	2	B24810	beta-conglycinin a
10	859.5	24.3	605	N	S20007	beta-conglycinin a
11	855.5	24.2	605	سز	FWSYBA	beta-conglycinin a
12	832.5	23.6	571		S00566	convicilin precurs
13	798	22.6	524		JQ1730	62K sucrose-bindin
14	770.5	21.8	483		T06459	62K sucrose-bindin
15	765	21.7	448		S24756	vicilin-like stora
16	760.5	21.5	433	N	S00567	vicilin precursor
17	760.5	21.5	459	N	S08505	vicilin - garden p
18	749.5	21.2	438	ν	S35757	vicilin, 47K - gar
19	748	21.2	439	_	FWSYCB	beta-conglycinin b
20	727	20.6	450	2	S15675	globulin-2 precurs
21	715.5	20.3	463	N	A27288	vicilin precursor
22	711.5	20.1	463	ν	806309	vicilin precursor
23	704.5	19.9	410	۳	<b>FWPMVB</b>	vicilin B precurso
24	689.5	19.5	445	N	JQ2264	canavalin - jack b
25	682.5	19.3	445	Ν	S00281	٠
26	568	16.1	436	ν	A23498	۲ <u>۰</u>
27	565	16.0	430	2	S10156	alpha-phaseolin pr
28	557	15.8	421	2	A24810	phaseolin beta cha
٥		,				vicilin - Zamia fo

413

ERFSERSELLKGIKNORLALLEARPHTFIVPHHLDAECVLLVVRGRATITTVVQEKRETR 472

## ALIGNMENTS

protein PV100 [imported] - winter squash (C;Species: Cucurbita maxima (winter squash) C;Cspecies: Cucurbita maxima (winter squash) C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000 C;Accession: T44430 #sequence\_revision M: Nishimura, M: Hara-Nishimura, I.

Biol. Chem. 274, 2563-2570, 1999
A;Fitle: Multiple functional proteins are produced by cleaving Asn-Gln bonds of a sin A;Reference number: Z22767; MUID:99107919
A;Reference number: T44430
A;Ression: T44430
A;Ression: T44430
A;Ressidues: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Ressidues: 1-810 -<YAM>
A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062 δõ 멍 Qy Вþ DЬ Qy ф 20 Ъ δõ Вр Qy Вþ Query Match
Best Local Similarity
Matches 284; Conserv 274 ENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNR----353 228 293 196 DCRRRCEQQE-----233 RRGGRDDEDENQRDPDWRREQKRREQEQERRERERRGGRDDEDENQRDPDWRREQERREQ 154 179 121 94 99 61 32 ------DRQEYEECKRQCMQLETS-GQMRRCVSQCDKRFEE--------- $\vdash$ SGPRQQQYCQRRCKEICEEEEEYNRQRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERR 153 ERRDPEWERSEQRRREHEREERRRRERERERGRGRRDENERDPKREQEERQR---REQE 178 ERRREREQERREREHRGGRDVEDENQRDPDWRREQERRREEEQREREWEREHGRRGRE Y-----EKE-----KRKQQKRYEEQQREDEEKYEERMKEEDNKRDP-----QQREYE 195 RRRREQEQRERERRGERDEEDDEN-QRDPDWRREQ-----ERREQERRRREQEQERRERQ ---DIDWSKY-----DNQDDPQTDCQQCQRRCRQQE 93 ACKKGCGVNQRGSPRAEYEVCRLRCQVAERGVEQQRKCEQVCEERLREREQGRGEDVDEV 120 MALSKVKLRLCLLAFTLFLACLSVGLGDKGESLSSGAGVDHDGCVNRCEELKGKNVDEFA 60 EQRSREDERRRHERQHGGRSRVNQVAIRRTEQEQSNNPYYFQEQRFQSRYRSDEGHWRVL 412 ------DLINPQRGGSGRYEE-----GEEKQSDNPYYFDERSLSTRFRTEEGHISVL 33.7%; Score 1191.5; DB 2; Length 810; milarity 34.3%; Pred. No. 1.6e-66; Conservative 144; Mismatches 218; Indels 183; Gaps 273 352 227 292 232 65 23;

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C;Keywords: seed; storage protein F;1-24/Domain: signal seenence F; 25-566/Droad
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A;Introns: 211/1; 269/3; 296/3; 391/3; 502/1
C;Superfamily: 9lycinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Theobroma cacao (cacao)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: S22477; S22478; S18105; S22050
R;McHenry, L.; Fritz, P.J.
Plant Mol. Biol. 18, 1173-1176, 1992
A:Title: Comparison of the structure and nucleotide sequence of A;Reference number: S22477; MUID:92288309
A:Accession: S22477
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A; Residues: 1-452 < MC2>
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S22477
vicilin precursor
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A; Accession: S22478
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A; Residues: 1-566 <MCH>
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Best Local
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5-566/Product: vicilin #status predicted <MAT>
     343
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 IPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAAL
                                                         LRALKNYRLVLLEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIR 342
                                                                                                             ER-GEHENYHNHKKNRSEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPP 175
                                                                                                                                  GRGGDLINPQRGGSGRYEEGEEKQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKL
                                                                                                                                                                                      KEQQRQQEEEL----
                                                                                                                                                                                                                                                                LCSGVSAYGRKQYERDPRQQYEQCQRRCESEATEEREQEQCEQRCER---
                                                                                                                                                                                                                EEQQREDEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQE--PRQQYQCQRRCREQQRQH 223
                                        LKGINDYRLAMFEANPNTFILPHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KREAIVVPVGHPVVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPY
                                                                                                                                                                                                                                                                                    ICEEEEEYNR*---QRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVEGKQADEIFRSQRESFFTEGPEGGRRRST---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STKVVVVASGEADVEMACPHLS-----GRHGGRRGGKRHEEEE-----DVHYEQVKARLS
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                                                                                                                                                                                                                                                                                                                                       al Similarity 41.1
237; Conservative
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                                                                                                                                                                                                                                                                                                                                         106;
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Pred. No. 1.2e
06; Mismatches
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C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed emba; Reference number: $06398
A; Accession: $06398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Gossypium hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar
C:Accession: S06398
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A; Residues: 1-605 <CHL>
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                                                         LEANPNAEVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTEYLIN 353
RDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVL
                                    LEANPNTFVLPHHCDAEKIYVVTNGRGTVTFVTHENKESYNVVPGVVVRIPAGSTVYLAN
                                                                                                                                                                                      NKWREEEEEES----
                                                                                                                                                                                                                      EKYEERMKEEDNKRDPOOREYEDCRRRCEOOEPROOYOCORRCREOOROHGRGGDLINPO 233
                                                                                                                                                                                                                                                                                             EEYNRQRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDE 173
                                                                                                                                                                                                                                                                                                                                  Q---DKCEDRSETQLKEEQQRDGEDPQRRYQDCRQHCQQEERRLRP-----HCEQSCREQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                               MAINTSNLCSLLFLLSLFLLSTTVSLAE-----SEFD-RQEYEECKRQCMQLETSGQMR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVV 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPAGSTVYVVSQDNQEKLTIAVLALPVNSPGKYELFFPAGNNKPESYYGAFSYEVLETVF
                                                                                                                                                                                                                                                             YEKQQQQQPDKQFKECQQRCQWQEQRPERKQQCVKECREQYQEDPWKGER---
                                                                                                                                                                                                                                                                                                                                                                      RCVSQCDKRFEEDIDWSKYDNQDDPQTDCQQCQRRCRQQESGPRQQQYCQRRCKEICEEE 113
                                                                                                                                                                                                                                                                                                                                                                                                            MVRNKSVFVVLLE--SLFLSFGLLCSAKDFPGRRSEDDPQQRYEDCRKRC-QLETRGQTE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFNNPDESYFMSFSQQRQRGDER---RGNPLASILDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHAVTFFASKDQPLNAVAFGLNAQNNQRIFLAGK-KNLVRQMDSEAKELSFGVPSKLVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHPVVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDGYGYAQMACPHLSRQSQGSQSGRQDRREQEEESEEETFGEFQQVKAPLSPGDVFVAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASGEADVEMACPHLSGRHGGRRGGK--RHEEEEDV-----HYEQVKARLSKREAIVVPV
                                                                                                           -----DEGEQQQRNNPYYFHRRSFQERFREEHGNFRVLQRFADKHHLLRGINEFRIAI
                                                                                                                                             RGGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INLLSQSPVYSNQNGRFFEACPEDFSQFQNMDVAVSAFKLNQGAIFVPHYNSKATFVVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTQREKLEEILEEQRGQKRQQGQQGMFRKAKPEQIRAISQQATSPR----HRGGE--RLA
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alpha-globulin B precursor (clone C72) - upland cotton
N; Alternate names: seed storage protein; vicilin precursor
C; Species: Gossypium hirsutum (upland cotton)
C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C; Date: 30-Sep-1991 #text_change 16-Jul-1999
C; Date: 30-Sep-1991 #text_change 16-Jul-1999
C; Date: 30-Sep-1991 
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A; Reference number: S06398
A; Accession: S06911
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
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C; Comment: This is a seed storage protein.
C; Comment: This is a seed storage protein.
C; Comment: This is a seed storage protein.
C; Keywords: glycoprotein; seed; storage protein
C; Keywords: glycoprotein; seed; storage protein
C; F; 1-25/Domain: signal sequence #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DDPOTDCQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQYEQCQERC 133
KQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPT
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                                                                                                                                                                                                                                         R--QQEERQRPQCQQRCLKRFEQEQQQ
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                                                                                FQECQQHCHQQEQRPERKQQCVRECRERYQE - -
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A; Residues: 1-509 < CHL>
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alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N;Alternate names: seed storage protein
C:Species: Gossyplum hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: S08059
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A; Molecule type: protein
A; Residues: 87-100 <KRI>
C; Superfamily: glycinin
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A; Title: Characterization of embryo globulins
A; Reference number: A43642; MUID:89374022
A; Accession: A43642
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Genetics 129, 863-872, 1991
A:Title: Molecular basis for allelic polymorphism
A:Reference number: A53234; MUID:92090707
A:Accession: A53234
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C;Species: Zea mays (maize)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A53234; A43642
R;Belanger, F.C.; Kriz, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: inbred line Va 26 A; Note: sequence extracted from NCBI backbone
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A;Molecule type: DNA
A;Residues: 1-573 <BEL>
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SIANQHGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLYNTRSFKIAYVPNGKGYAE 378
                                   LYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVE 522
                                                                                                     RLRGVLGQ--QREGVIISASQEQIRELTRDDSE---SRRWHIRRGGESSRGPYNLENKRP 462
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                                                                              RLERLFGRHGQDKGIIVRATEEQTRELRRHASEGGHGPHWPLPPFGE-SRGPYSLLDQRP
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39.9%;
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94; Mismatches 180
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C:Species: Zea mays (maize)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: B53334; S21824
R:Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A:Title: Molecular basis for allelic polymorphism of the maize GA:Reference number: A53234; MUID:92090707
A:Accession: B53234
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A;Introns: 167/1; 225/3;
C;Superfamily: glycinin
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A;Note: sequence extracted from NCBI backbone (NCBIP:71285)
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A; Residues: 1-582 <BEL>
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AVASRDSNLQIVCFEVHADRNEKVFLAGAD-NVLQKLDRVAKALSFASKAEEVDEVLGSR
                                                                                                                                                                                                                  PHLSGRHG----GRRGGKRHEEEEDVH-----YEQVKARLSKREAIVVPVGHPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                            RLFGRHGQDKGIIVRATEEQTRELRRHASEGGHGPHWPLPPFGE-SRGPYSLLDQRPSIA
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                                                                                                                                              PHRQSQGGESERERDKGRRSEEEEEESSEEQEEAGQGYHTIRARLSPGTAFVVPAGHPFV
                                                                                                                                                                                                                                                                                             NQHGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLFNTRSFKIAYVPNGKGYAEIVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEGSSEDEREQEKEKQKDRRPYVFDRRSFRRVVRSEQGSLRVLRPFDEVSRLLRGIRDYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDDNHHHHGGHKSGQCVRRCEDRPWHQRPRCLEQCREEEREKRQERSRHEADD----RS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQDESIFFPGPRQ---HQQQSSRSTKQQQ 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVCPHRQSQGGESERERGKGRRSEEEEESSEEQEEVGQGYHTIRARLSPGTAFVVPAGHP
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Pred. No. 2.7e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 183;
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Beachy, R.N.; Slightom,

Phaseolus vulgaris

20-Aug-1999

PID:g169929 as Glu

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RESULT 8
S35221
globulin Beg1 p
C; Species: Horo
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A;Reference number: S35221; MUID:93287988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Map position: 4
C:Superfamily: glycinin
C:Keywords: glycoprotein
F:174-190/Product: globulin Begl #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Hordeum vulgare (barley)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
C:Accession: S3521
C:Accession: S3521
R:Heck, G.R.; Chamberlain, A.K.; Ho, T.H.D.
Mol. Gen. Genet. 239, 209-218, 1993
Mol. Gen. Genet. 239, 209-218, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-637 <HEC>
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nes 227; Conserv
    APRKEVEELFNSQDESI-FFPGPRQHQQQSSRSTKQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          AFVVPPGHPVVEISSSQGSSNLQVVCFEINAERNERVWLAGR-NNVIGKLGSPAQELTFG
                                                                                                            AIVVPVGHPVVFVSS--GNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFA 618
                                                                                                                                                       PHLGRESESEREHGK--GRRREEEEDDQRQQRRRGSESESEEEEEQQRYETVRARVSRGS
                                                                                                                                                                                                  PHL - - - - SGRHGGRRGGKRHEEEED - - - - - - -
                                                                                                                                                                                                                                             NRHGRLYEADARSFHALANQDVRVAVANITPGSMTAPYLNTQSFKLAVVLEGEGEVQIVC
                                                                                                                                                                                                                                                                                   NKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMAC
                                                                                                                                                                                                                                                                                                                                QRQGQEKTRSVSIVRASEEQLRELRREAAEGGQGHRWPLPPFRGDSRDTFNLLEQRPKIA
                                                                                                                                                                                                                                                                                                                                                                         QQ-----REGVIISASQEQIRELTRDDSE---SRRWHIRRGGESSRGPYNLFNKRPLYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVNPRAFVVPGFTDADGVGYVAQGEGVLTVIENGEKRSYTVKEGDVIVAPAGSIMHLANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEE-----KYEERMKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASHDDEDDRRGGHSLQQCVQRCRQER--PR---YSHARCVQEC------
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Pred. No. 5.3e-47;
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A:Title: The glycosylated seed storage proteins of Glycine max and A; Reference number: A24810; MUID:86250867
A; Accession: B24810
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C;Superfamily: glycinin
C;Keywords: seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA A; Residues: 361-639 . C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-conglycinin alpha chain precursor - soybean
C;Species: Glycine max (soybean)
C;Date: 07-Mar-1988 #sequence_revision 30-Jun-1991 #text_change
C;Accession: B24810; S16337
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A; Residues: 1-639 <DOY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKEEDNKRDPQQREYEDCRRRCEQQEPRQQYQCQRRCREQQRQHGRGGGLINPQRGGSGR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPQQQYEQCQ-ERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEER
                    KVVVVASGEADVEMACPHLSGRHGGRRGGKRHEEEED-VHYEQVKARLSKREAIVVPVGH
                                                                                                                                                                                                                                                                                                                            TLLLPHHADADYLIVILNGTAILTLYNNDDRDSYNLQSGDALRVPAGTTFYVVNPDNDEN
                                                                                                                                                                                                                                                                                                                                                    HKQEKHQGKESEEEEED-----QDEDEEQ-------DKESQESEGSES
                                                               SEDKPFNLGSRDPIYSNKLGKLFEITQRN-PQLRDLDVFLSVVDMNEGALFLPHFNSKAI
                                                                                                       SSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRST
                                                                                                                                                  SYDTKFEEINKVLFGREEGQQQGEERLQESVIVEISKKQIRELSKHAKSSSRKTI----S
                                                                                                                                                                                           ALNTQAERLRGVL-----GQQ-----REGVIISASQEQIRELTRDDSESRRWHIRRGGE
                                                                                                                                                                                                                                        LRMIAGTTFYVVNPDNDENLRMITLAIPVNKPGRFESFFLSSTQAQQSYLQGFSKNILEA
                                                                                                                                                                                                                                                                              ----AGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WSKYDNQDDPQTDCQQCQ-RRCRQQESGPRQQQYCQRRCKEICEEEE-----EYNRQR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----EEECEEGQIPRPRPQHPERERQQHGEK-----EEDEGEQPRPFPFPRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLLGVVFLASVSVSFGIAYWEKQNPSHNKCLRSCNSEKDSYRNQACHARCNLLKVEE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.7%; Score 872.5; DB 2; 30.7%; Pred. No. 7.7e-47; tive 147; Mismatches 226;
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344

163

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RESULT S20007

Ş g Qy В

В

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beta conglycinin alpha chain precursor - soybean
C:Species: Glycine max (soybean)
C;Dete: 19 Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-19
C:Accession: S20007
R;Lelievre, J.M.; Dickinson, C.D.; Dickinson, L.A.; Nielsen, N.C.
Plant Mol. Biol. 18, 259-274, 1992
A:Title: Synthesis and assembly of soybean beta-conglycinin in vitro.
A;Reference number: S20007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-605 <LEL>
C;Superfamily: 91ycinin
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Best Local :
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                                                                        FGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEELFNSQDESIFFPGPRQHQ
                                                                                                                                                                                                                                                   KYGQAYEVKPEDYRQLQDMDVSVFŢANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP
                                                                                                                                                                                                                                                                                                                                              -----GQQR--EGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                  ERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDNODDPQTDCQQCQRRCRQQESGPRQQQYCQRRC-----KEICEEEE---EYNRQRDP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSQSESYFVDAQPQQKEEGNKGRK--GPLSSIL
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QQSSRSTKQQQPLVSIL
                                              IGINAENNQRNFLAGSQDNVISQIPSQVQELAFPGSAQAVEKLLKNQRESYFVDAQPKKK
                                                                                                                                                                               HLSGRHGG--RRGGKRHEEEEDVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLFA
                                                                                                                                                                                                                           KLGKFFEITPEKNPQLRDLDIFLSIVDMNEGALLLPHFNSKAIVILVINEGDANIELV---
                                                                                                                                                                                                                                                                                                                    EGQQQGEQRLQESVIVEISKEQIRALSKRAKSSSRKTI----SSEDKPFNLRSRDPIYSN
                                                                                                                                                                                                                                                                                                                                                                                                           ENLRLITLAIPVNKPGRFESFFLSSTEAQQSYLQGFSRNILEASYDTKFEEINKVLFSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNTLLLPNHADADYLIVILNGTAILSLVNNDDRDSYRLQSGDALRVPSGTTYYVVNPDNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDEEQDERQFPFP---RPPHQKEERKQEEDED--EEQQRES---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDNKRDPQQREYEDCRRRCEQQEPRQQYQCQRRCREQQRQHGRGGDLINPQRGGSGRYEE 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YWEKENPKHN--KCLQSCNSERDSYRNQA-CHARCNLLKVEKEECEEGEIPRPRPRPQHP
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195; Conser
                                                                                                                                  -GLKEQQQEQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVV---NATSNLNFFA
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Pred. No. 4.0
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ches 210;
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A;Molecule type: protein
A;Residues: 189-196,'H',198,'N',200,'X',202-203;397-408,'X',410,'X',412-417,'X',419-4
A;Experimental source: seed
C;Superfamily: glycinin
C;Keywords: glycoprotein; seed; storage protein
C;Keywords: glycoprotein; seed; storage protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-62/Domain: propeptide #status predicted <PRO>
F;36-605/Product: beta-conglycinin alpha chain #status predicted <MAT>
F;61,517/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Title: Limited proteolysis of beta-conglycinin and glycinin, A;Reference number: $74123; MUID:97054613
A;Accession: $74124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-605 <SEB>
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                                                                                                                                                                                                         -----GQQR--EGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSN
                                                                                                                                                                                                                                                                                                 ERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVL----
                                                                                                                                                                                                                                                                                                                                                                                          PNAEVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTEYLINRDNN
                                          HLSGRHGG--RRGGKRHEEEEDVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLFA 584
                                                                                                             KYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVVASGEADVEMACP
                                                                                                                                                                             EGQQQGEQRLQESVIVEISKEQIRALSKRAKSSSRKTI----SSEDKPFNLRSRDPIYSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YWEKENPKHN--KCLQSCNSERDSYRNQA-CHARCNLLKVEKEECEEGE1PRPRPRPQHP
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                                                                                        KLGKFFETTPEKNPQLRDLDTFLSTVDMNEGALLLPHFNSKAIVILVINEGDANTELV--
-GLKEQQQEQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVV--NATSNLNFFA
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A:Map position: 2
A:Introns: 221/1; 279/3; 304/3; 412/3; 507/1
C:Superfamily: 91yoinin
E:1-28/Domain: signal sequence #status predicted <SIG>
E:29-571/Product: convicilin #status experimental <MAT
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C; Geneti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  convicilin precursor (clone pJC4) - garden pea (Species: Pisum sativum (garden pea) C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 C;Accession: S00566 R;Bown, D.; Ellis, T.H.N.; Gatehouse, J.A. Biochem. J. 251, 717-726, 1998 A;Title: The sequence of a gene encoding convicilin A;Reference number: S00566; MUID:88326208 A;Accession: S00566
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A; Residues: 1-571 <BOW>
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S00566
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Best Local Similarity 32.7
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                                                  GKLFEITPEKKYPOLODLDILVSCVEINKGALMLPHYNSRAIVVLLVNEGKGNLELL---
                                                                         GQAYEVKPE-DYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPH
                                                                                                                       KRTQQGEERD-AIIKVSREQIEELRKLAKSSS----KKSLPSEFEPFNLRSHKPEYSNKF
                                                                                                                                                                                        PVNRPGKFEAF--GLSENKNQYLRGFSKNILEASLNTKYETIEKVLLEEQEKKPQQLRDR
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                                                                                                                                                      -GOQREGVIISASQEQIRELTRODSESRRWHIRRGGESSRGPYNLFNKRPLYSNKY
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Pred. No. 2e-4
10; Mismatches
-DVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENL
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C;Accession: JQ1730
R;Grimes, H.D.; Overvoorde, P.J.; Ripp, K.; Francescut, R;Grimes, H.D.; Overvoorde, P.J.; Ripp, K.; Francescut, R;Grimes, H.D.; Overvoorde, P.J.; Ripp, K.; Francescut, M.; Plant Cell 4, 1561-1574, 1992
A;Title: A 62-kD sucrose binding protein is expressed and A:Daference number: JQ1730; MUID:93104680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-524 <GRI>
A; Cross references: GB:L06038;
C; Superfamily: alvoinin
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JO1730
62K sucrose-binding protein precursor - soybean
C:Species: Glycine max (soybean)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
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C;Keywords: sugar transport
F;1-29/Domain: signal sequence #status predicted
F;30-524/Product: 62K sucrose-binding protein #s
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                                                ENLLMICFEVNARDNKKFTFAGKD-NIVSSLDNVAKELAFNYPSEMVNGVFLLQRFLERK
                                                                              ENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEELF---
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Pred. No. 2.6e-42;
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submitted to the EMBL Data Library, February 1997
A;Reference number: Z15693
A;Accession: T06459
A;Status: preliminary; translated from GB/EMBL/DDB3
A;Molecule type: mRNA
A;Residues: 1 -483 <ROD>
A;Cross references: EMBL:Y11207; pIDN:CAA72090.1
A;Experimental source: var. Lincoln
C;Genetics:
A;Note: p54
C;Superfamily: glycinin
N;Alternate names: P54 protein homolog - C;Species: Pisum sativum (garden pea) C;Date: 23-Apr-1999 #sequence_revision C;Accession: T06459 R;Rodrigo II, M.T
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62K sucrose-binding
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Best Local S
Matches 163
                                                                                                                                                                         442
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                                                                                                                                                                                                       QAMELAFAAPRKEVEELFNSQDESIFFPGPRQHQQQ 646
                                                                                                                                                                                                                                                                                                        LANITKGSMSTIHYNTNANKIALVIDGEGELEMACPHMPSSSSNSR-----QKKSSISYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF---LQTIST 371
                                                                                                                                                                         AAKEVAFDIAAEKVDEVFERKEE-FFFPYDNEERKE
                                                                                                                                                                                                                                        NINAKLRPGVMFVVPAGHPFVNIASKKKNLIVVCFEVNAQRNKKLALAGK-KNIVSALDK
                                                                                                                                                                                                                                                                         QVKARLSKREAIVVPVGHPVVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEP 610
                                                                                                                                                                                                                                                                                                                                         IANITQGSMMGPFFNTRSTKVVVVVASGEADVEMACPHLSGRHGGRRGGKRHEEEEDVHYE 550
                                                                                                                                                                                                                                                                                                                                                                          LAPKKS----LWPF----GGPFKSPFNIFSNNPAFSNKFGSLEEVGPSQEKSGLEGLNLMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVLGQQREGVIISASQEQIRE 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIKGRGIIGLVAEDRTERFNLEEGDIMRVPAGTPMYLVNRDENEKLYIAAFHMPPSSGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDADAILL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RICMERCD-----DYIKKKQERQKHKEH------EEEEEQEQEEDENPYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQREY 194
                                                                                                                                                                                                                                                                                                                                                                                                           LTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQ-LQDMDVSVF 490
                                                                                                                                                                                                                                                                                                                                                                                                                                            PVNLEPFFESAGRKPESVLNTFSSKVLQAALKSSKGELETVLDEQKKGRIFKIEKEDVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDNDFETKIDTKDGRVLILNKFNEKSKLLKNIENYGLAVLEIKANAFLSPHHYDSEAILF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDCRRRCEQQEPROQYQCQRRCREQQRQHGRGGDLINPQRGGSGRYEEGEEKQSDNPYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKEKDP-ELTTCKDQCD-----MQRQYDEEDK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 770.5; DB 2
Pred. No. 1.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 garden
                                                   10-Sep-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-Apr-1999 #text_change 20-Jun-2000
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                                                     10-Sep-1999
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A;Accession: S24756
A;Molecule type: mRNA
A;Residues: 1-448 <NEW>
A;Cross-references: EMBL:X63191; NID:g20500; PIDN:CAA44873.1; PID:g20501
C;Superfamily: vicilin
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Best Local
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                                                                                                                                                                                                                                                                     GVLGQQREGVIISASQEQIRELTRDDSESRRWHIRRG---GESSR----GPYNLFNKRPL 463
HQQQSSRST
                                   WFDLNTRGNERQFLAGK-NNVLNTLEREIRQLSFNVPRGEEIEEVLQAQKDQVILRGPQR
                                                                  AFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPR-KEVEELFNSQDESIFFPGPRQ 642
                                                                                                                                                                                                                                                RIFGGHKSGVIIHANEEQIREMMR------KRGFSAGSMSAPEHPKPFNLRNQKPD
                                                                                                                                                                                                                                                                                                                     VNNDDHNTLRIASLVRPVSTVRGEYQPFYVAGGRNPQTVYSAFSDDVLEAAFNTNVQQLE
                                                                                                                                                                                                                                                                                                                                                      INRDNNERLHIAKFLQTIST-PGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLR 410
                                                                                                                                                                                                                                                                                                                                                                                                                            VLLEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEYLGRGRGRR-EEEREENPYVFHSDSFRTRASSEAGEIRALPNFGEVSELLEGIRKFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PORGGSGRYEEGEEKOSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRL
                                                                                                     ACPHL-GQHGW--SSPRERGDQDITYQRVWAKLRTGSVYIVPAGHPITEIASTNSRLQIL
                                                                                                                                         ACPHLSGRHGGRRGGKRHEEEEDVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLF
                                                                                                                                                                            FENENGRETIAGPKNYPFLDALDVSVGLADLNPGSMTAPSLNSKSTSIGIVTNGEGRIEM
                                                                                                                                                                                                             YSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEM
                                                                                                                                                                                                                                                                                                                                                                                           TCIEMKPNTVMLPHYIDATWILYVTRGRGYIAYVHQNELVKRKLEEGDVFGVPSGHTFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 765; DB 1;
Pred. No. 2.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 448
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                                   438
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